

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/140,729ADATE: 03/04/94
TIME: 11:22:03

INPUT SET: S7433.raw

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Amara, Susan G
Arriza, Jeffrey L

(ii) TITLE OF INVENTION: Amino Acid Transporters and Uses

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Allegretti & Witcoff, Ltd.
(B) STREET: 10 South Wacker Drive, Suite 3000
(C) CITY: Chicago
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60606

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/140,729
(B) FILING DATE: 20 OCT 1993
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Noonan, Kevin E
(B) REGISTRATION NUMBER: 35,303
(C) REFERENCE/DOCKET NUMBER: 93,509

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 312-715-1000
(B) TELEFAX: 312-715-1234
(C) TELEX: 910-221-5317

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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52
53
54     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
55
56     CTGRGCRATG AARATGGCAG CCAGGGCYTC ATACAGGGCT GTGCCRTCCA TGTTTRATGGT      60
57
58     RGC                                                                    63
59
60     (2) INFORMATION FOR SEQ ID NO:2:
61
62         (i) SEQUENCE CHARACTERISTICS:
63             (A) LENGTH: 1680 base pairs
64             (B) TYPE: nucleic acid
65             (C) STRANDEDNESS: single
66             (D) TOPOLOGY: linear
67
68         (ii) MOLECULE TYPE: cDNA
69
70         (ix) FEATURE:
71             (A) NAME/KEY: 5'UTR
72             (B) LOCATION: 1..30
73
74         (ix) FEATURE:
75             (A) NAME/KEY: CDS
76             (B) LOCATION: 31..1626
77
78         (ix) FEATURE:
79             (A) NAME/KEY: 3'UTR
80             (B) LOCATION: 1626..1680
81
82
83     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
84
85     CACCTCTAGC TCGGAGCGGC GTGTAGCGCC ATG GAG AAG AGC AAC GAG ACC AAC      54
86                                     Met Glu Lys Ser Asn Glu Thr Asn
87                                     1           5
88
89     GGC TAC CTT GAC AGC GCT CAG GCG GGG CCT GCG GCC GGG CCC GGA GCT      102
90     Gly Tyr Leu Asp Ser Ala Gln Ala Gly Pro Ala Ala Gly Pro Gly Ala
91         10           15           20
92
93     CCG GGG ACC GCG GCG GGA CGC GCA CGG CGT TGC GCG CGC TTC CTG CGG      150
94     Pro Gly Thr Ala Ala Gly Arg Ala Arg Arg Cys Ala Arg Phe Leu Arg
95         25           30           35           40
96
97     CGC CAA GCG CTG GTG CTG CTC ACC GTG TCC GGG GTG CTG GCG GGC GCG      198
98     Arg Gln Ala Leu Val Leu Leu Thr Val Ser Gly Val Leu Ala Gly Ala
99         45           50           55
100
101     GGC CTG GGC GCG GCG TTG CGC GGG CTC AGC CTG AGC CGC ACG CAG GTC      246
102     Gly Leu Gly Ala Ala Leu Arg Gly Leu Ser Leu Ser Arg Thr Gln Val

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103		60		65		70											
104																	
105	ACC	TAC	CTG	GCC	TTC	CCC	GGC	GAG	ATG	CTG	CTC	CGC	ATG	CTG	CGC	ATG	294
106	Thr	Tyr	Leu	Ala	Phe	Pro	Gly	Glu	Met	Leu	Leu	Arg	Met	Leu	Arg	Met	
107			75					80					85				
108																	
109	ATC	ATC	CTG	CCG	CTG	GTG	GTC	TGC	AGC	CTG	GTG	TCG	GGC	GCC	GCC	TCG	342
110	Ile	Ile	Leu	Pro	Leu	Val	Val	Cys	Ser	Leu	Val	Ser	Gly	Ala	Ala	Ser	
111			90					95					100				
112																	
113	CTC	GAT	GCC	AGC	TGC	CTC	GGG	CGT	CTG	GGC	GGC	ATC	CGT	GTC	GCC	TAC	390
114	Leu	Asp	Ala	Ser	Cys	Leu	Gly	Arg	Leu	Gly	Gly	Ile	Arg	Val	Ala	Tyr	
115	105						110				115					120	
116																	
117	TTT	GGC	CTC	ACC	ACA	CTG	AGT	GCC	TCG	GCG	CTC	GCC	GTG	GCC	TTG	GCG	438
118	Phe	Gly	Leu	Thr	Thr	Leu	Ser	Ala	Ser	Ala	Leu	Ala	Val	Ala	Leu	Ala	
119					125					130				135			
120																	
121	TTC	ATC	ATC	AAG	CCA	GGA	TCC	GGT	GCG	CAG	ACC	CTT	CAG	TCC	AGC	GAC	486
122	Phe	Ile	Ile	Lys	Pro	Gly	Ser	Gly	Ala	Gln	Thr	Leu	Gln	Ser	Ser	Asp	
123				140					145					150			
124																	
125	CTG	GGG	CTG	GAG	GAC	TCG	GGG	CCT	CCT	CCT	GTC	CCC	AAA	GAG	ACG	GTG	534
126	Leu	Gly	Leu	Glu	Asp	Ser	Gly	Pro	Pro	Pro	Val	Pro	Lys	Glu	Thr	Val	
127			155					160					165				
128																	
129	GAC	TCT	TTC	CTC	GAC	CTG	GCC	AGA	AAC	CTG	TTT	CCC	TCC	AAT	CTT	GTG	582
130	Asp	Ser	Phe	Leu	Asp	Leu	Ala	Arg	Asn	Leu	Phe	Pro	Ser	Asn	Leu	Val	
131			170				175					180					
132																	
133	GTT	GCA	GCT	TTC	CGT	ACG	TAT	GCA	ACC	GAT	TAT	AAA	GTC	GTG	ACC	CAG	630
134	Val	Ala	Ala	Phe	Arg	Thr	Tyr	Ala	Thr	Asp	Tyr	Lys	Val	Val	Thr	Gln	
135	185					190					195					200	
136																	
137	AAC	AGC	AGC	TCT	GGA	AAT	GTA	ACC	CAT	GAA	AAG	ATC	CCC	ATA	GGC	ACT	678
138	Asn	Ser	Ser	Ser	Gly	Asn	Val	Thr	His	Glu	Lys	Ile	Pro	Ile	Gly	Thr	
139				205					210					215			
140																	
141	GAG	ATA	GAA	GGG	ATG	AAC	ATT	TTA	GGA	TTG	GTC	CTG	TTT	GCT	CTG	GTG	726
142	Glu	Ile	Glu	Gly	Met	Asn	Ile	Leu	Gly	Leu	Val	Leu	Phe	Ala	Leu	Val	
143				220					225					230			
144																	
145	TTA	GGA	GTG	GCC	TTA	AAG	AAA	CTA	GGC	TCC	GAA	GGA	GAA	GAC	CTC	ATC	774
146	Leu	Gly	Val	Ala	Leu	Lys	Lys	Leu	Gly	Ser	Glu	Gly	Glu	Asp	Leu	Ile	
147			235					240					245				
148																	
149	CGT	TTC	TTC	AAT	TCC	CTC	AAC	GAG	GCG	ACG	ATG	GTG	CTG	GTG	TCC	TGG	822
150	Arg	Phe	Phe	Asn	Ser	Leu	Asn	Glu	Ala	Thr	Met	Val	Leu	Val	Ser	Trp	
151		250					255					260					
152																	
153	ATT	ATG	TGG	TAC	GTA	CCT	GTG	GGC	ATC	ATG	TTC	CTT	GTT	GGA	AGC	AAG	870

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154	Ile Met Trp Tyr Val Pro Val Gly Ile Met Phe Leu Val Gly Ser Lys	
155	265 270 275 280	
156		
157	ATC GTG GAA ATG AAA GAC ATC ATC GTG CTG GTG ACC AGC CTG GGG AAA	918
158	Ile Val Glu Met Lys Asp Ile Ile Val Leu Val Thr Ser Leu Gly Lys	
159	285 290 295	
160		
161	TAC ATC TTC GCA TCT ATA TTG GGC CAT GTT ATT CAT GGA GGA ATT GTT	966
162	Tyr Ile Phe Ala Ser Ile Leu Gly His Val Ile His Gly Gly Ile Val	
163	300 305 310	
164		
165	CTG CCA CTT ATT TAT TTT GTT TTC ACA CGA AAA AAC CCA TTC AGA TTC	1014
166	Leu Pro Leu Ile Tyr Phe Val Phe Thr Arg Lys Asn Pro Phe Arg Phe	
167	315 320 325	
168		
169	CTC CTG GGC CTC CTC GCC CCA TTT GCG ACA GCA TTT GCT ACC TGC TCC	1062
170	Leu Leu Gly Leu Leu Ala Pro Phe Ala Thr Ala Phe Ala Thr Cys Ser	
171	330 335 340	
172		
173	AGC TCA GCG ACC CTT CCC TCT ATG ATG AAG TGC ATT GAA GAG AAC AAT	1110
174	Ser Ser Ala Thr Leu Pro Ser Met Met Lys Cys Ile Glu Glu Asn Asn	
175	345 350 355 360	
176		
177	GGT GTG GAC AAG AGG ATC AGC AGG TTT ATT CTC CCC ATC GGG GCC ACC	1158
178	Gly Val Asp Lys Arg Ile Ser Arg Phe Ile Leu Pro Ile Gly Ala Thr	
179	365 370 375	
180		
181	GTG AAC ATG GAC GGA GCA GCC ATC TTC CAG TGT GTG GCC GCG GTG TTC	1206
182	Val Asn Met Asp Gly Ala Ala Ile Phe Gln Cys Val Ala Ala Val Phe	
183	380 385 390	
184		
185	ATT GCG CAA CTC AAC AAC ATA GAG CTC AAC GCA GGA CAG ATT TTC ACC	1254
186	Ile Ala Gln Leu Asn Asn Ile Glu Leu Asn Ala Gly Gln Ile Phe Thr	
187	395 400 405	
188		
189	ATT CTA GTG ACT GCC ACA GCG TCC AGT GTT GGA GCA GCA GGC GTG CCA	1302
190	Ile Leu Val Thr Ala Thr Ala Ser Ser Val Gly Ala Ala Gly Val Pro	
191	410 415 420	
192		
193	GCT GGA GGG GTC CTC ACC ATT GCC ATT ATC CTG GAG GCC ATT GGG CTG	1350
194	Ala Gly Gly Val Leu Thr Ile Ala Ile Ile Leu Glu Ala Ile Gly Leu	
195	425 430 435 440	
196		
197	CCT ACT CAT GAC CTG CCT CTG ATC CTG GCT GTG GAC TGG ATT GTG GAC	1398
198	Pro Thr His Asp Leu Pro Leu Ile Leu Ala Val Asp Trp Ile Val Asp	
199	445 450 455	
200		
201	CGG ACC ACC ACG GTG GTG AAT GTG GAG GGG GAT GCC CTG GGT GCA GGC	1446
202	Arg Thr Thr Thr Val Val Asn Val Glu Gly Asp Ala Leu Gly Ala Gly	
203	460 465 470	
204		

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205  ATT CTC CAC CAC CTG AAT CAG AAG GCA ACA AAG AAA GGC GAG CAG GAA      1494
206  Ile Leu His His Leu Asn Gln Lys Ala Thr Lys Lys Gly Glu Gln Glu
207          475                      480                      485
208
209  CTT GCT GAG GTG AAA GTG GAA GCC ATC CCC AAC TGC AAG TCT GAG GAG      1542
210  Leu Ala Glu Val Lys Val Glu Ala Ile Pro Asn Cys Lys Ser Glu Glu
211      490                      495                      500
212
213  GAG ACA TCG CCC CTG GTG ACA CAC CAG AAC CCC GCT GGC CCC GTG GCC      1590
214  Glu Thr Ser Pro Leu Val Thr His Gln Asn Pro Ala Gly Pro Val Ala
215  505                      510                      515                      520
216
217  AGT GCC CCA GAA CTG GAA TCC AAG GAG TCG GTT CTG TGATGGGGCT      1636
218  Ser Ala Pro Glu Leu Glu Ser Lys Glu Ser Val Leu
219          525                      530
220
221  GGGCTTTGGG CTTGCCTGCC AGCAGTGATG TCCCACCCTG TTCA      1680
222
223
224  (2) INFORMATION FOR SEQ ID NO:3:
225
226      (i) SEQUENCE CHARACTERISTICS:
227          (A) LENGTH: 532 amino acids
228          (B) TYPE: amino acid
229          (D) TOPOLOGY: linear
230
231      (ii) MOLECULE TYPE: protein
232
233      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
234
235  Met Glu Lys Ser Asn Glu Thr Asn Gly Tyr Leu Asp Ser Ala Gln Ala
236      1                      5                      10                      15
237
238  Gly Pro Ala Ala Gly Pro Gly Ala Pro Gly Thr Ala Ala Gly Arg Ala
239          20                      25                      30
240
241  Arg Arg Cys Ala Arg Phe Leu Arg Arg Gln Ala Leu Val Leu Leu Thr
242          35                      40                      45
243
244  Val Ser Gly Val Leu Ala Gly Ala Gly Leu Gly Ala Ala Leu Arg Gly
245          50                      55                      60
246
247  Leu Ser Leu Ser Arg Thr Gln Val Thr Tyr Leu Ala Phe Pro Gly Glu
248      65                      70                      75                      80
249
250  Met Leu Leu Arg Met Leu Arg Met Ile Ile Leu Pro Leu Val Val Cys
251          85                      90                      95
252
253  Ser Leu Val Ser Gly Ala Ala Ser Leu Asp Ala Ser Cys Leu Gly Arg
254          100                     105                     110
255

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INPUT SET: S7433.raw

256	Leu	Gly	Gly	Ile	Arg	Val	Ala	Tyr	Phe	Gly	Leu	Thr	Thr	Leu	Ser	Ala
257			115					120					125			
258																
259	Ser	Ala	Leu	Ala	Val	Ala	Leu	Ala	Phe	Ile	Ile	Lys	Pro	Gly	Ser	Gly
260		130					135					140				
261																
262	Ala	Gln	Thr	Leu	Gln	Ser	Ser	Asp	Leu	Gly	Leu	Glu	Asp	Ser	Gly	Pro
263	145					150					155					160
264																
265	Pro	Pro	Val	Pro	Lys	Glu	Thr	Val	Asp	Ser	Phe	Leu	Asp	Leu	Ala	Arg
266					165					170					175	
267																
268	Asn	Leu	Phe	Pro	Ser	Asn	Leu	Val	Val	Ala	Ala	Phe	Arg	Thr	Tyr	Ala
269				180					185					190		
270																
271	Thr	Asp	Tyr	Lys	Val	Val	Thr	Gln	Asn	Ser	Ser	Ser	Gly	Asn	Val	Thr
272			195					200					205			
273																
274	His	Glu	Lys	Ile	Pro	Ile	Gly	Thr	Glu	Ile	Glu	Gly	Met	Asn	Ile	Leu
275		210					215					220				
276																
277	Gly	Leu	Val	Leu	Phe	Ala	Leu	Val	Leu	Gly	Val	Ala	Leu	Lys	Lys	Leu
278	225					230					235					240
279																
280	Gly	Ser	Glu	Gly	Glu	Asp	Leu	Ile	Arg	Phe	Phe	Asn	Ser	Leu	Asn	Glu
281					245					250					255	
282																
283	Ala	Thr	Met	Val	Leu	Val	Ser	Trp	Ile	Met	Trp	Tyr	Val	Pro	Val	Gly
284				260					265					270		
285																
286	Ile	Met	Phe	Leu	Val	Gly	Ser	Lys	Ile	Val	Glu	Met	Lys	Asp	Ile	Ile
287			275					280					285			
288																
289	Val	Leu	Val	Thr	Ser	Leu	Gly	Lys	Tyr	Ile	Phe	Ala	Ser	Ile	Leu	Gly
290		290					295					300				
291																
292	His	Val	Ile	His	Gly	Gly	Ile	Val	Leu	Pro	Leu	Ile	Tyr	Phe	Val	Phe
293	305					310					315					320
294																
295	Thr	Arg	Lys	Asn	Pro	Phe	Arg	Phe	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Phe
296				325						330					335	
297																
298	Ala	Thr	Ala	Phe	Ala	Thr	Cys	Ser	Ser	Ser	Ala	Thr	Leu	Pro	Ser	Met
299				340					345					350		
300</																

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307 Phe Gln Cys Val Ala Ala Val Phe Ile Ala Gln Leu Asn Asn Ile Glu
308 385 390 395 400
309
310 Leu Asn Ala Gly Gln Ile Phe Thr Ile Leu Val Thr Ala Thr Ala Ser
311 405 410 415
312
313
314 Ser Val Gly Ala Ala Gly Val Pro Ala Gly Gly Val Leu Thr Ile Ala
315 420 425 430
316
317 Ile Ile Leu Glu Ala Ile Gly Leu Pro Thr His Asp Leu Pro Leu Ile
318 435 440 445
319
320 Leu Ala Val Asp Trp Ile Val Asp Arg Thr Thr Thr Val Val Asn Val
321 450 455 460
322
323 Glu Gly Asp Ala Leu Gly Ala Gly Ile Leu His His Leu Asn Gln Lys
324 465 470 475 480
325
326 Ala Thr Lys Lys Gly Glu Gln Glu Leu Ala Glu Val Lys Val Glu Ala
327 485 490 495
328
329 Ile Pro Asn Cys Lys Ser Glu Glu Glu Thr Ser Pro Leu Val Thr His
330 500 505 510
331
332 Gln Asn Pro Ala Gly Pro Val Ala Ser Ala Pro Glu Leu Glu Ser Lys
333 515 520 525
334
335 Glu Ser Val Leu
336 530
337

(2) INFORMATION FOR SEQ ID NO:4:

338
339
340 (i) SEQUENCE CHARACTERISTICS:
341 (A) LENGTH: 1680 base pairs
342 (B) TYPE: nucleic acid
343 (C) STRANDEDNESS: single
344 (D) TOPOLOGY: linear
345
346 (ii) MOLECULE TYPE: cDNA
347
348 (ix) FEATURE:
349 (A) NAME/KEY: 5'UTR
350 (B) LOCATION: 1..30
351
352 (ix) FEATURE:
353 (A) NAME/KEY: CDS
354 (B) LOCATION: 31..1656
355
356 (ix) FEATURE:
357 (A) NAME/KEY: 3'UTR

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358             (B) LOCATION: 1657..1680
359
360             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
361
362 AAAGAAGAGA CCCTCCTAGA AAAGTAAAAT ATG ACT AAA AGC AAT GGA GAA GAG      54
363             Met Thr Lys Ser Asn Gly Glu Glu
364             1             5
365
366 CCC AAG ATG GGG GGC AGG ATG GAG AGA TTC CAG CAG GGA GTC CGT AAA      102
367 Pro Lys Met Gly Gly Arg Met Glu Arg Phe Gln Gln Gly Val Arg Lys
368     10             15             20
369
370 CGC ACA CTT TTG GCC AAG AAG AAA GTG CAG AAC ATT ACA AAG GAG GTT      150
371 Arg Thr Leu Leu Ala Lys Lys Lys Val Gln Asn Ile Thr Lys Glu Val
372     25             30             35             40
373
374 GTT AAA AGT TAC CTG TTT CGG AAT GCT TTT GTG CTG CTC ACA GTC ACC      198
375 Val Lys Ser Tyr Leu Phe Arg Asn Ala Phe Val Leu Leu Thr Val Thr
376             45             50             55
377
378 GCT GTC ATT GTG GGT ACA ATC CTT GGA TTT ACC CTC CGA CCA TAC AGA      246
379 Ala Val Ile Val Gly Thr Ile Leu Gly Phe Thr Leu Arg Pro Tyr Arg
380             60             65             70
381
382 ATG AGC TAC CGG GAA GTC AAG TAC TTC TCC TTT CCT GGG GAA CTT CTG      294
383 Met Ser Tyr Arg Glu Val Lys Tyr Phe Ser Phe Pro Gly Glu Leu Leu
384             75             80             85
385
386 ATG AGG ATG TTA CAG ATG CTG GTC TTA CCA CTT ATC ATC TCC AGT CTT      342
387 Met Arg Met Leu Gln Met Leu Val Leu Pro Leu Ile Ile Ser Ser Leu
388     90             95             100
389
390 GTC ACA GGA ATG GCG GCG CTA GAT AGT AAG GCA TCA GGG AAG TGG GAA      390
391 Val Thr Gly Met Ala Ala Leu Asp Ser Lys Ala Ser Gly Lys Trp Glu
392    105             110             115             120
393
394 TGC GGA GCT GTA GTC TAT TAT ATG ACT ACC ACC ATC ATT GCT GTG GTG      438
395 Cys Gly Ala Val Val Tyr Tyr Met Thr Thr Thr Ile Ile Ala Val Val
396             125             130             135
397
398 ATT GGC ATA ATC ATT GTC ATC ATC ATC CAT CCT GGG AAG GGC ACA AAG      486
399 Ile Gly Ile Ile Ile Val Ile Ile Ile His Pro Gly Lys Gly Thr Lys
400             140             145             150
401
402 GAA AAC ATG CAC AGA GAA GGC AAA ATT GTA CGA GTG ACA GCT GCA GAT      534
403 Glu Asn Met His Arg Glu Gly Lys Ile Val Arg Val Thr Ala Ala Asp
404             155             160             165
405
406 GCC TTC CTG GAC TTG ATC AGG AAC ATG TTA AAT CCA AAT CTG GTA GAA      582
407 Ala Phe Leu Asp Leu Ile Arg Asn Met Leu Asn Pro Asn Leu Val Glu
408     170             175             180

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409																		
410	GCC	TGC	TTT	AAA	CAG	TTT	AAA	ACC	AAC	TAT	GAG	AAG	AGA	AGC	TTT	AAA		630
411	Ala	Cys	Phe	Lys	Gln	Phe	Lys	Thr	Asn	Tyr	Glu	Lys	Arg	Ser	Phe	Lys		
412	185					190					195					200		
413																		
414	GTG	CCC	ATC	CAG	GCC	AAC	GAA	ACG	CTT	GTG	GGT	GCT	GTG	ATA	AAC	AAT		678
415	Val	Pro	Ile	Gln	Ala	Asn	Glu	Thr	Leu	Val	Gly	Ala	Val	Ile	Asn	Asn		
416					205					210					215			
417																		
418	GTG	TCT	GAG	GCC	ATG	GAG	ACT	CTT	ACC	CGA	ATC	ACA	GAG	GAG	CTG	GTC		726
419	Val	Ser	Glu	Ala	Met	Glu	Thr	Leu	Thr	Arg	Ile	Thr	Glu	Glu	Leu	Val		
420				220					225					230				
421																		
422	CCA	GTT	CCA	GGA	TCT	GTG	AAT	GGA	GTC	AAT	GCC	CTG	GGT	CTA	GTT	GTC		774
423	Pro	Val	Pro	Gly	Ser	Val	Asn	Gly	Val	Asn	Ala	Leu	Gly	Leu	Val	Val		
424			235					240				245						
425																		
426	TTC	TCC	ATG	TGC	TTC	GGT	TTT	GTG	ATT	GGA	AAC	ATG	AAG	GAA	CAG	GGG		822
427	Phe	Ser	Met	Cys	Phe	Gly	Phe	Val	Ile	Gly	Asn	Met	Lys	Glu	Gln	Gly		
428		250					255					260						
429																		
430	CAG	GCC	CTG	AGA	GAG	TTC	TTT	GAT	TCT	CTT	AAC	GAA	GCC	ATC	ATG	AGA		870
431	Gln	Ala	Leu	Arg	Glu	Phe	Phe	Asp	Ser	Leu	Asn	Glu	Ala	Ile	Met	Arg		
432	265					270					275					280		
433																		
434	CTG	GTA	GCA	GTA	ATA	ATG	TGG	TAT	GCC	CCC	GTG	GGT	ATT	CTC	TTC	CTG		918
435	Leu	Val	Ala	Val	Ile	Met	Trp	Tyr	Ala	Pro	Val	Gly	Ile	Leu	Phe	Leu		
436					285					290					295			
437																		
438	ATT	GCT	GGG	AAG	ATT	GTG	GAG	ATG	GAA	GAC	ATG	GGT	GTG	ATT	GGG	GGG		966
439	Ile	Ala	Gly	Lys	Ile	Val	Glu	Met	Glu	Asp	Met	Gly	Val	Ile	Gly	Gly		
440				300					305					310				
441																		
442	CAG	CTT	GCC	ATG	TAC	ACC	GTG	ACT	GTC	ATT	GTT	GGC	TTA	CTC	ATT	CAC		1014
443	Gln	Leu	Ala	Met	Tyr	Thr	Val	Thr	Val	Ile	Val	Gly	Leu	Leu	Ile	His		
444			315					320					325					
445																		
446	GCA	GTC	ATC	GTC	TTG	CCA	CTC	CTC	TAC	TTC	TTG	GTA	ACA	CGG	AAA	AAC		1062
447	Ala	Val	Ile	Val	Leu													

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460          380          385          390
461
462   GTA GGA GCC ACC ATT AAC ATG GAT GGG ACT GCC CTC TAT GAG GCT TTG      1254
463   Val Gly Ala Thr Ile Asn Met Asp Gly Thr Ala Leu Tyr Glu Ala Leu
464          395          400          405
465
466   GCT GCC ATT TTC ATT GCT CAA GTT AAC AAC TTT GAA CTG AAC TTC GGA      1302
467   Ala Ala Ile Phe Ile Ala Gln Val Asn Asn Phe Glu Leu Asn Phe Gly
468          410          415          420
469
470   CAA ATT ATT ACA ATC AGC ATC ACA GCC ACA GCT GCC AGT ATT GGG GCA      1350
471   Gln Ile Ile Thr Ile Ser Ile Thr Ala Thr Ala Ala Ser Ile Gly Ala
472   425          430          435          440
473
474   GCT GGA ATT CCT CAG GCG GGC CTG GTC ACT ATG GTC ATT GTG CTG ACA      1398
475   Ala Gly Ile Pro Gln Ala Gly Leu Val Thr Met Val Ile Val Leu Thr
476          445          450          455
477
478   TCT GTC GGC CTG CCC ACT GAC GAC ATC ACG CTC ATC ATC GCG GTG GAC      1446
479   Ser Val Gly Leu Pro Thr Asp Asp Ile Thr Leu Ile Ile Ala Val Asp
480          460          465          470
481
482   TGG TTC TTG GAT CGC CTC CGG ACC ACC ACC AAC GTA CTG GGA GAC TCC      1494
483   Trp Phe Leu Asp Arg Leu Arg Thr Thr Thr Asn Val Leu Gly Asp Ser
484          475          480          485
485
486   CTG GGA GCT GGG ATT GTG GAG CAC TTG TCA CGA CAT GAA CTG AAG AAC      1542
487   Leu Gly Ala Gly Ile Val Glu His Leu Ser Arg His Glu Leu Lys Asn
488          490          495          500
489
490   AGA GAT GTT GAA ATG GGT AAC TCA GTG ATT GAA GAG AAT GAA ATG AAG      1590
491   Arg Asp Val Glu Met Gly Asn Ser Val Ile Glu Glu Asn Glu Met Lys
492   505          510          515          520
493
494   AAA CCA TAT CAA CTG ATT GCA CAG GAC AAT GAA ACT GAG AAA CCC ATC      1638
495   Lys Pro Tyr Gln Leu Ile Ala Gln Asp Asn Glu Thr Glu Lys Pro Ile
496          525          530          535
497
498   GAC AGT GAA ACC AAG ATG TAGACTAACA TAAAGAAACA CTTT      1680
499   Asp Ser Glu Thr Lys Met
500          540
501
502

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 542 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

RAW SEQUENCE LISTING PATENT APPLICATION US/08/140,729A

DATE: 03/04/94
TIME: 11:23:08

INPUT SET: S7433.raw

```

511
512      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
513
514  Met Thr Lys Ser Asn Gly Glu Glu Pro Lys Met Gly Gly Arg Met Glu
515      1              5              10              15
516
517  Arg Phe Gln Gln Gly Val Arg Lys Arg Thr Leu Leu Ala Lys Lys Lys
518              20              25              30
519
520  Val Gln Asn Ile Thr Lys Glu Val Val Lys Ser Tyr Leu Phe Arg Asn
521              35              40              45
522
523  Ala Phe Val Leu Leu Thr Val Thr Ala Val Ile Val Gly Thr Ile Leu
524              50              55              60
525
526  Gly Phe Thr Leu Arg Pro Tyr Arg Met Ser Tyr Arg Glu Val Lys Tyr
527      65              70              75              80
528
529  Phe Ser Phe Pro Gly Glu Leu Leu Met Arg Met Leu Gln Met Leu Val
530              85              90              95
531
532  Leu Pro Leu Ile Ile Ser Ser Leu Val Thr Gly Met Ala Ala Leu Asp
533              100             105             110
534
535  Ser Lys Ala Ser Gly Lys Trp Glu Cys Gly Ala Val Val Tyr Tyr Met
536              115             120             125
537
538  Thr Thr Thr Ile Ile Ala Val Val Ile Gly Ile Ile Ile Val Ile Ile
539      130             135             140
540
541  Ile His Pro Gly Lys Gly Thr Lys Glu Asn Met His Arg Glu Gly Lys
542      145             150             155             160
543
544  Ile Val Arg Val Thr Ala Ala Asp Ala Phe Leu Asp Leu Ile Arg Asn
545              165             170             175
546
547  Met Leu Asn Pro Asn Leu Val Glu Ala Cys Phe Lys Gln Phe Lys Thr
548              180             185             190
549
550  Asn Tyr Glu Lys Arg Ser Phe Lys Val Pro Ile Gln Ala Asn Glu Thr
551              195             200             205
552
553  Leu Val Gly Ala Val Ile Asn Asn Val Ser Glu Ala Met Glu Thr Leu
554      210             215             220
555
556  Thr Arg Ile Thr Glu Glu Leu Val Pro Val Pro Gly Ser Val Asn Gly
557      225             230             235             240
558
559  Val Asn Ala Leu Gly Leu Val Val Phe Ser Met Cys Phe Gly Phe Val
560              245             250             255
561

```

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/140,729A

 DATE: 03/04/94
 TIME: 11:23:14
INPUT SET: S7433.raw

```

562   Ile Gly Asn Met Lys Glu Gln Gly Gln Ala Leu Arg Glu Phe Phe Asp
563           260                      265                      270
564
565   Ser Leu Asn Glu Ala Ile Met Arg Leu Val Ala Val Ile Met Trp Tyr
566           275                      280                      285
567
568   Ala Pro Val Gly Ile Leu Phe Leu Ile Ala Gly Lys Ile Val Glu Met
569           290                      295                      300
570
571   Glu Asp Met Gly Val Ile Gly Gly Gln Leu Ala Met Tyr Thr Val Thr
572   305                      310                      315                      320
573
574
575   Val Ile Val Gly Leu Leu Ile His Ala Val Ile Val Leu Pro Leu Leu
576           325                      330                      335
577
578   Tyr Phe Leu Val Thr Arg Lys Asn Pro Trp Val Phe Ile Gly Gly Leu
579           340                      345                      350
580
581   Leu Gln Ala Leu Ile Thr Ala Leu Gly Thr Ser Ser Ser Ser Ala Thr
582           355                      360                      365
583
584   Leu Pro Ile Thr Phe Lys Cys Leu Glu Glu Asn Asn Gly Val Asp Lys
585           370                      375                      380
586
587   Arg Val Thr Arg Phe Val Leu Pro Val Gly Ala Thr Ile Asn Met Asp
588   385                      390                      395                      400
589
590   Gly Thr Ala Leu Tyr Glu Ala Leu Ala Ala Ile Phe Ile Ala Gln Val
591           405                      410                      415
592
593   Asn Asn Phe Glu Leu Asn Phe Gly Gln Ile Ile Thr Ile Ser Ile Thr
594           420                      425                      430
595
596   Ala Thr Ala Ala Ser Ile Gly Ala Ala Gly Ile Pro Gln Ala Gly Leu
597           435                      440                      445
598
599   Val Thr Met Val Ile Val Leu Thr Ser Val Gly Leu Pro Thr Asp Asp
600           450                      455                      460
601
602   Ile Thr Leu Ile Ile Ala Val Asp Trp Phe Leu Asp Arg Leu Arg Thr
603   465                      470                      475                      480
604
605   Thr Thr Asn Val Leu Gly Asp Ser Leu Gly Ala Gly Ile Val Glu His
606           485                      490                      495
607
608   Leu Ser Arg His Glu Leu Lys Asn Arg Asp Val Glu Met Gly Asn Ser
609           500                      505                      510
610
611   Val Ile Glu Glu Asn Glu Met Lys Lys Pro Tyr Gln Leu Ile Ala Gln
612           515                      520                      525

```

RAW SEQUENCE LISTING PATENT APPLICATION US/08/140,729A

DATE: 03/04/94
TIME: 11:23:21

INPUT SET: S7433.raw

```

613
614 Asp Asn Glu Thr Glu Lys Pro Ile Asp Ser Glu Thr Lys Met
615      530                      535                      540
616
617
618 (2) INFORMATION FOR SEQ ID NO:6:
619
620 (i) SEQUENCE CHARACTERISTICS:
621 (A) LENGTH: 1800 base pairs
622 (B) TYPE: nucleic acid
623 (C) STRANDEDNESS: single
624 (D) TOPOLOGY: linear
625
626 (ii) MOLECULE TYPE: cDNA
627
628 (ix) FEATURE:
629 (A) NAME/KEY: 5'UTR
630 (B) LOCATION: 1..33
631
632 (ix) FEATURE:
633 (A) NAME/KEY: CDS
634 (B) LOCATION: 34..1755
635
636 (ix) FEATURE:
637 (A) NAME/KEY: 3'UTR
638 (B) LOCATION: 1756..1800
639
640 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
641
642 GATAGTGCTG AAGAGGAGGG GCGTTCCCAG ACC ATG GCA TCT ACG GAA GGT GCC      54
643                               Met Ala Ser Thr Glu Gly Ala
644                               1                      5
645
646 AAC AAT ATG CCC AAG CAG GTG GAA GTG CGA ATG CCA GAC AGT CAT CTT      102
647 Asn Asn Met Pro Lys Gln Val Glu Val Arg Met Pro Asp Ser His Leu
648      10                      15                      20
649
650 GGC TCA GAG GAA CCC AAG CAC CGG CAC CTG GGC CTG CGC CTG TGT GAC      150
651 Gly Ser Glu Glu Pro Lys His Arg His Leu Gly Leu Arg Leu Cys Asp
652      25                      30                      35
653
654 AAG CTG GGG AAG AAT CTG CTG CTC ACC CTG ACG GTG TTT GGT GTC ATC      198
655 Lys Leu Gly Lys Asn Leu Leu Leu Thr Leu Thr Val Phe Gly Val Ile
656      40                      45                      50                      55
657
658 CTG GGA GCA GTG TGT GGA GGG CTT CTT CGC TTG GCA TCT CCC ATC CAC      246
659 Leu Gly Ala Val Cys Gly Gly Leu Leu Arg Leu Ala Ser Pro Ile His
660                      60                      65                      70
661
662 CCT GAT GTG GTT ATG TTA ATA GCC TTC CCA GGG GAT ATA CTC ATG AGG      294
663 Pro Asp Val Val Met Leu Ile Ala Phe Pro Gly Asp Ile Leu Met Arg

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/140,729A

DATE: 03/04/94
TIME: 11:23:27

INPUT SET: S7433.raw

664		75		80		85		
665								
666	ATG CTA AAA ATG CTC ATT CTG GGT CTA ATC ATC TCC AGC TTA ATC ACA							342
667	Met Leu Lys Met Leu Ile Leu Gly Leu Ile Ile Ser Ser Leu Ile Thr							
668		90		95		100		
669								
670	GGG TTG TCA GGC CTG GAT GCT AAG GCT AGT GGC CGC TTG GGC ACG AGA							390
671	Gly Leu Ser Gly Leu Asp Ala Lys Ala Ser Gly Arg Leu Gly Thr Arg							
672		105		110		115		
673								
674	GCC ATG GTG TAT TAC ATG TCC ACG ACC ATC ATT GCT GCA GTA CTG GGG							438
675	Ala Met Val Tyr Tyr Met Ser Thr Thr Ile Ile Ala Ala Val Leu Gly							
676		120		125		130		135
677								
678	GTC ATT CTG GTC TTG GCT ATC CAT CCA GGC AAT CCC AAG CTC AAG AAG							486
679	Val Ile Leu Val Leu Ala Ile His Pro Gly Asn Pro Lys Leu Lys Lys							
680		140		145		150		
681								
682	CAG CTG GGC CCT GGC AAG AAG AAT GAT GAA GTG TCC AGC CTG GAT GCC							534
683	Gln Leu Gly Pro Gly Lys Lys Asn Asp Glu Val Ser Ser Leu Asp Ala							
684		155		160		165		
685								
686	TTC CTG GAC CTT ATT CGA AAT CTC TTC CCT GAA AAC CTT GTC CAA GCC							582
687	Phe Leu Asp Leu Ile Arg Asn Leu Phe Pro Glu Asn Leu Val Gln Ala							
688		170		175		180		
689								
690	TGC TTT CAA CAG ATT CAA ACA GTG ACG AAG AAA GTC CTG GTT GCA CCA							630
691	Cys Phe Gln Gln Ile Gln Thr Val Thr Lys Lys Val Leu Val Ala Pro							
692		185		190		195		
693								
694	CCG CCA GAC GAG GAG GCC AAC GCA ACC AGC GCT GAA GTC TCT CTG TTG							678
695	Pro Pro Asp Glu Glu Ala Asn Ala Thr Ser Ala Glu Val Ser Leu Leu							
696		200		205		210		215
697								
698	AAC GAG ACT GTG ACT GAG GTG CCG GAG GAG ACT AAG ATG GTT ATC AAG							726
699	Asn Glu Thr Val Thr Glu Val Pro Glu Glu Thr Lys Met Val Ile Lys							
700		220		225		230		
701								
702	AAG GGC CTG GAG TTC AAG GAT GGG ATG AAC GTC TTA GGT CTG ATA GGG							774
703	Lys Gly Leu Glu Phe Lys Asp Gly Met Asn Val Leu Gly Leu Ile Gly							
704		235		240		245		
705								
706	TTT TTC ATT GCT TTT GGC ATC GCT ATG GGG AAG ATG GGA GAT CAG GCC							822
707	Phe Phe Ile Ala Phe Gly Ile Ala Met Gly Lys Met Gly Asp Gln Ala							
708		250		255		260		
709								
710	AAG CTG ATG GTG GAT TTC TTC AAC ATT TTG AAT GAG ATT GTA ATG AAG							870
711	Lys Leu Met Val Asp Phe Phe Asn Ile Leu Asn Glu Ile Val Met Lys							
712		265		270		275		
713								
714	TTA GTG ATC ATG ATC ATG TGG TAC TCT CCC CTG GGT ATC GCC TGC CTG							918

RAW SEQUENCE LISTING PATENT APPLICATION US/08/140,729A

DATE: 03/04/94
TIME: 11:23:34

INPUT SET: S7433.raw

715	Leu Val Ile Met Ile Met Trp Tyr Ser Pro Leu Gly Ile Ala Cys Leu	
716	280 285 290 295	
717		
718	ATC TGT GGA AAG ATC ATT GCA ATC AAG GAC TTA GAA GTG GTT GCT AGG	966
719	Ile Cys Gly Lys Ile Ile Ala Ile Lys Asp Leu Glu Val Val Ala Arg	
720	300 305 310	
721		
722	CAA CTG GGG ATG TAC ATG GTA ACA GTG ATC ATA GGC CTC ATC ATC CAC	1014
723	Gln Leu Gly Met Tyr Met Val Thr Val Ile Ile Gly Leu Ile Ile His	
724	315 320 325	
725		
726	GGG GGC ATC TTT CTC CCC TTG ATT TAC TTT GTA GTG ACC AGG AAA AAC	1062
727	Gly Gly Ile Phe Leu Pro Leu Ile Tyr Phe Val Val Thr Arg Lys Asn	
728	330 335 340	
729		
730	CCC TTC TCC CTT TTT GCT GGC ATT TTC CAA GCT TGG ATC ACT GCC CTG	1110
731	Pro Phe Ser Leu Phe Ala Gly Ile Phe Gln Ala Trp Ile Thr Ala Leu	
732	345 350 355	
733		
734	GGC ACC GCT TCC AGT GCT GGA ACT TTG CCT GTC ACC TTT CGT TGC CTG	1158
735	Gly Thr Ala Ser Ser Ala Gly Thr Leu Pro Val Thr Phe Arg Cys Leu	
736	360 365 370 375	
737		
738	GAA GAA AAT CTG GGG ATT GAT AAG CGT GTG ACT AGA TTC GTC CTT CCT	1206
739	Glu Glu Asn Leu Gly Ile Asp Lys Arg Val Thr Arg Phe Val Leu Pro	
740	380 385 390	
741		
742	GTT GGA GCA ACC ATT AAC ATG GAT GGT ACA GCC CTT TAT GAA GCG GTG	1254
743	Val Gly Ala Thr Ile Asn Met Asp Gly Thr Ala Leu Tyr Glu Ala Val	
744	395 400 405	
745		
746	GCC GCC ATC TTT ATA GCC CAA ATG AAT GGT GTT GTC CTG GAT GGA GGA	1302
747	Ala Ala Ile Phe Ile Ala Gln Met Asn Gly Val Val Leu Asp Gly Gly	
748	410 415 420	
749		
750	CAG ATT GTG ACT GTA AGC CTC ACA GCC ACC CTG GCA AGC GTC GGC GCG	1350
751	Gln Ile Val Thr Val Ser Leu Thr Ala Thr Leu Ala Ser Val Gly Ala	
752	425 430 435	
753		
754	GCC AGT ATC CCC AGT GCC GGG CTG GTC ACC ATG CTC CTC ATT CTG ACA	1398
755	Ala Ser Ile Pro Ser Ala Gly Leu Val Thr Met Leu Leu Ile Leu Thr	
756	440 445 450 455	
757		
758	GCC GTG GGC CTG CCA ACA GAG GAC ATC AGC TTG CTG GTG GCT GTG GAC	1446
759	Ala Val Gly Leu Pro Thr Glu Asp Ile Ser Leu Leu Val Ala Val Asp	
760	460 465 470	
761		
762	TGG CTG CTG GAC AGG ATG AGA ACT TCA GTC AAT GTT GTG GGT GAC TCT	1494
763	Trp Leu Leu Asp Arg Met Arg Thr Ser Val Asn Val Val Gly Asp Ser	
764	475 480 485	
765		

RAW SEQUENCE LISTING PATENT APPLICATION US/08/140,729A

DATE: 03/04/94
TIME: 11:23:40

INPUT SET: S7433.raw

```

766   TTT GGG GCT GGG ATA GTC TAT CAC CTC TCC AAG TCT GAG CTG GAT ACC      1542
767   Phe Gly Ala Gly Ile Val Tyr His Leu Ser Lys Ser Glu Leu Asp Thr
768           490                      495                      500
769
770   ATT GAC TCC CAG CAT CGA GTG CAT GAA GAT ATT GAA ATG ACC AAG ACT      1590
771   Ile Asp Ser Gln His Arg Val His Glu Asp Ile Glu Met Thr Lys Thr
772           505                      510                      515
773
774   CAA TCC ATT TAT GAT GAC ATG AAG AAC CAC AGG GAA AGC AAC TCT AAT      1638
775   Gln Ser Ile Tyr Asp Asp Met Lys Asn His Arg Glu Ser Asn Ser Asn
776   520                      525                      530                      535
777
778   CAA TGT GTC TAT GCT GCA CAC AAC TCT GTC ATA GTA GAT GAA TGC AAG      1686
779   Gln Cys Val Tyr Ala Ala His Asn Ser Val Ile Val Asp Glu Cys Lys
780           540                      545                      550
781
782   GTA ACT CTG GCA GCC AAT GGA AAG TCA GCC GAC TGC AGT GTT GAG GAA      1734
783   Val Thr Leu Ala Ala Asn Gly Lys Ser Ala Asp Cys Ser Val Glu Glu
784           555                      560                      565
785
786   GAA CCT TGG AAA CGT GAG AAA TAAGGATATG AGTCTCAGCA AATTCTTGAA      1785
787   Glu Pro Trp Lys Arg Glu Lys
788           570
789
790   TAAACTCCCC AGCGT      1800
791
792
793   (2) INFORMATION FOR SEQ ID NO:7:
794
795       (i) SEQUENCE CHARACTERISTICS:
796           (A) LENGTH: 574 amino acids
797           (B) TYPE: amino acid
798           (D) TOPOLOGY: linear
799
800       (ii) MOLECULE TYPE: protein
801
802       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
803
804   Met Ala Ser Thr Glu Gly Ala Asn Asn Met Pro Lys Gln Val Glu Val
805       1                      5                      10                      15
806
807   Arg Met Pro Asp Ser His Leu Gly Ser Glu Glu Pro Lys His Arg His
808       20                      25                      30
809
810   Leu Gly Leu Arg Leu Cys Asp Lys Leu Gly Lys Asn Leu Leu Leu Thr
811       35                      40                      45
812
813   Leu Thr Val Phe Gly Val Ile Leu Gly Ala Val Cys Gly Gly Leu Leu
814       50                      55                      60
815
816   Arg Leu Ala Ser Pro Ile His Pro Asp Val Val Met Leu Ile Ala Phe

```


RAW SEQUENCE LISTING PATENT APPLICATION US/08/140,729A

DATE: 03/04/94
TIME: 11:23:46

INPUT SET: S7433.raw

817	65		70		75		80
818							
819	Pro Gly Asp Ile Leu Met Arg Met Leu Lys Met Leu Ile Leu Gly Leu						
820		85		90		95	
821							
822	Ile Ile Ser Ser Leu Ile Thr Gly Leu Ser Gly Leu Asp Ala Lys Ala						
823		100		105		110	
824							
825	Ser Gly Arg Leu Gly Thr Arg Ala Met Val Tyr Tyr Met Ser Thr Thr						
826		115		120		125	
827							
828	Ile Ile Ala Ala Val Leu Gly Val Ile Leu Val Leu Ala Ile His Pro						
829		130		135		140	
830							
831	Gly Asn Pro Lys Leu Lys Lys Gln Leu Gly Pro Gly Lys Lys Asn Asp						
832		145		150		155	160
833							
834	Glu Val Ser Ser Leu Asp Ala Phe Leu Asp Leu Ile Arg Asn Leu Phe						
835		165		170		175	
836							
837	Pro Glu Asn Leu Val Gln Ala Cys Phe Gln Gln Ile Gln Thr Val Thr						
838		180		185		190	
839							
840	Lys Lys Val Leu Val Ala Pro Pro Pro Asp Glu Glu Ala Asn Ala Thr						
841		195		200		205	
842							
843	Ser Ala Glu Val Ser Leu Leu Asn Glu Thr Val Thr Glu Val Pro Glu						
844		210		215		220	
845							
846	Glu Thr Lys Met Val Ile Lys Lys Gly Leu Glu Phe Lys Asp Gly Met						
847		225		230		235	240
848							
849	Asn Val Leu Gly Leu Ile Gly Phe Phe Ile Ala Phe Gly Ile Ala Met						
850		245		250		255	
851							
852	Gly Lys Met Gly Asp Gln Ala Lys Leu Met Val Asp Phe Phe Asn Ile						
853		260		265		270	
854							
855	Leu Asn Glu Ile Val Met Lys Leu Val Ile Met Ile Met Trp Tyr Ser						
856		275		280		285	
857							
858	Pro Leu Gly Ile Ala Cys Leu Ile Cys Gly Lys Ile Ile Ala Ile Lys						
859		290		295		300	
860							
861	Asp Leu Glu Val Val Ala Arg Gln Leu Gly Met Tyr Met Val Thr Val						
862		305		310		315	320
863							
864	Ile Ile Gly Leu Ile Ile His Gly Gly Ile Phe Leu Pro Leu Ile Tyr						
865		325		330		335	
866							
867	Phe Val Val Thr Arg Lys Asn Pro Phe Ser Leu Phe Ala Gly Ile Phe						

RAW SEQUENCE LISTING PATENT APPLICATION US/08/140,729A

DATE: 03/04/94
TIME: 11:23:53

INPUT SET: S7433.raw

```

868          340          345          350
869
870 Gln Ala Trp Ile Thr Ala Leu Gly Thr Ala Ser Ser Ala Gly Thr Leu
871          355          360          365
872
873
874 Pro Val Thr Phe Arg Cys Leu Glu Glu Asn Leu Gly Ile Asp Lys Arg
875          370          375          380
876
877 Val Thr Arg Phe Val Leu Pro Val Gly Ala Thr Ile Asn Met Asp Gly
878          385          390          395          400
879
880 Thr Ala Leu Tyr Glu Ala Val Ala Ala Ile Phe Ile Ala Gln Met Asn
881          405          410          415
882
883 Gly Val Val Leu Asp Gly Gly Gln Ile Val Thr Val Ser Leu Thr Ala
884          420          425          430
885
886 Thr Leu Ala Ser Val Gly Ala Ala Ser Ile Pro Ser Ala Gly Leu Val
887          435          440          445
888
889 Thr Met Leu Leu Ile Leu Thr Ala Val Gly Leu Pro Thr Glu Asp Ile
890          450          455          460
891
892 Ser Leu Leu Val Ala Val Asp Trp Leu Leu Asp Arg Met Arg Thr Ser
893          465          470          475          480
894
895 Val Asn Val Val Gly Asp Ser Phe Gly Ala Gly Ile Val Tyr His Leu
896          485          490          495
897
898 Ser Lys Ser Glu Leu Asp Thr Ile Asp Ser Gln His Arg Val His Glu
899          500          505          510
900
901 Asp Ile Glu Met Thr Lys Thr Gln Ser Ile Tyr Asp Asp Met Lys Asn
902          515          520          525
903
904 His Arg Glu Ser Asn Ser Asn Gln Cys Val Tyr Ala Ala His Asn Ser
905          530          535          540
906
907 Val Ile Val Asp Glu Cys Lys Val Thr Leu Ala Ala Asn Gly Lys Ser
908          545          550          555          560
909
910 Ala Asp Cys Ser Val Glu Glu Glu Pro Trp Lys Arg Glu Lys
911          565          570
912

```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1674 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/140,729ADATE: 03/04/94
TIME: 11:23:59

INPUT SET: S7433.raw

919 (D) TOPOLOGY: linear
920
921 (ii) MOLECULE TYPE: cDNA
922
923 (ix) FEATURE:
924 (A) NAME/KEY: 5'UTR
925 (B) LOCATION: 1..15
926
927 (ix) FEATURE:
928 (A) NAME/KEY: CDS
929 (B) LOCATION: 16..1590
930
931 (ix) FEATURE:
932 (A) NAME/KEY: 3'UTR
933 (B) LOCATION: 1591..1674
934
935
936 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
937
938 ATAGCGGCGA CAGCC ATG GGG AAA CCG GCG AGG AAA GGA TGC CCG AGT TGG 51
939 Met Gly Lys Pro Ala Arg Lys Gly Cys Pro Ser Trp
940 1 5 10
941
942 AAG CGC TTC CTG AAG AAT AAC TGG GTG TTG CTG TCC ACC GTG GCC GCG 99
943 Lys Arg Phe Leu Lys Asn Asn Trp Val Leu Leu Ser Thr Val Ala Ala
944 15 20 25
945
946 GTG GTG CTA GGC ATT ACC ACA GGA GTC TTG GTT CGA GAA CAC AGC AAC 147
947 Val Val Leu Gly Ile Thr Thr Gly Val Leu Val Arg Glu His Ser Asn
948 30 35 40
949
950 CTC TCA ACT CTA GAG AAA TTC TAC TTT GCT TTT CCT GGA GAA ATT CTA 195
951 Leu Ser Thr Leu Glu Lys Phe Tyr Phe Ala Phe Pro Gly Glu Ile Leu
952 45 50 55 60
953
954 ATG CGG ATG CTG AAA CTC ATC ATT TTG CCA TTA ATT ATA TCC AGC ATG 243
955 Met Arg Met Leu Lys Leu Ile Ile Leu Pro Leu Ile Ile Ser Ser Met
956 65 70 75
957
958 ATT ACA GGT GTT GCT GCA CTG GAT TCC AAC GTA TCC GGA AAA ATT GGT 291
959 Ile Thr Gly Val Ala Ala Leu Asp Ser Asn Val Ser Gly Lys Ile Gly
960 80 85 90
961
962 CTG CGC GCT GTC GTG TAT TAT TTC TGT ACC ACT CTC ATT GCT GTT ATT 339
963 Leu Arg Ala Val Val Tyr Tyr Phe Cys Thr Thr Leu Ile Ala Val Ile
964 95 100 105
965
966 CTA GGT ATT GTG CTG GTG GTG AGC ATC AAG CCT GGT GTC ACC CAG AAA 387
967 Leu Gly Ile Val Leu Val Val Ser Ile Lys Pro Gly Val Thr Gln Lys
968 110 115 120
969

RAW SEQUENCE LISTING PATENT APPLICATION US/08/140,729A

DATE: 03/04/94
TIME: 11:24:06

INPUT SET: S7433.raw

970	GTG GGT GAA ATT GCG AGG ACA GGC AGC ACC CCT GAA GTC AGT ACG GTG	435
971	Val Gly Glu Ile Ala Arg Thr Gly Ser Thr Pro Glu Val Ser Thr Val	
972	125 130 135 140	
973		
974	GAT GCC ATG TTA GAT CTC ATC AGG AAT ATG TTC CCT GAG AAT CTT GTC	483
975	Asp Ala Met Leu Asp Leu Ile Arg Asn Met Phe Pro Glu Asn Leu Val	
976	145 150 155	
977		
978	CAG GCC TGT TTT CAG CAG TAC AAA ACT AAG CGT GAA GAA GTG AAG CCT	531
979	Gln Ala Cys Phe Gln Gln Tyr Lys Thr Lys Arg Glu Glu Val Lys Pro	
980	160 165 170	
981		
982	CCC AGC GAT CCA GAG ATG AAC ATG ACA GAA GAG TCC TTC ACA GCT GTC	579
983	Pro Ser Asp Pro Glu Met Asn Met Thr Glu Glu Ser Phe Thr Ala Val	
984	175 180 185	
985		
986	ATG ACA ACT GCA ATT TCC AAG AAC AAA ACA AAG GAA TAC AAA ATT GTT	627
987	Met Thr Thr Ala Ile Ser Lys Asn Lys Thr Lys Glu Tyr Lys Ile Val	
988	190 195 200	
989		
990	GGC ATG TAT TCA GAT GGC ATA AAC GTC CTG GGC TTG ATT GTC TTT TGC	675
991	Gly Met Tyr Ser Asp Gly Ile Asn Val Leu Gly Leu Ile Val Phe Cys	
992	205 210 215 220	
993		
994	CTT GTC TTT GGA CTT GTC ATT GGA AAA ATG GGA GAA AAG GGA CAA ATT	723
995	Leu Val Phe Gly Leu Val Ile Gly Lys Met Gly Glu Lys Gly Gln Ile	
996	225 230 235	
997		
998	CTG GTG GAT TTC TTC AAT GCT TTG AGT GAT GCA ACC ATG AAA ATC GTT	771
999	Leu Val Asp Phe Phe Asn Ala Leu Ser Asp Ala Thr Met Lys Ile Val	
1000	240 245 250	
1001		
1002	CAG ATC ATC ATG TGT TAT ATG CCA CTA GGT ATT TTG TTC CTG ATT GCT	819
1003	Gln Ile Ile Met Cys Tyr Met Pro Leu Gly Ile Leu Phe Leu Ile Ala	
1004	255 260 265	
1005		
1006	GGG AAG ATC ATA GAA GTT GAA GAC TGG GAA ATA TTC CGC AAG CTG GGC	867
1007	Gly Lys Ile Ile Glu Val Glu Asp Trp Glu Ile Phe Arg Lys Leu Gly	
1008	270 275 280	
1009		
1010	CTT TAC ATG GCC ACA GTC CTG ACT GGG CTT GCA ATC CAC TCC ATT GTA	915
1011	Leu Tyr Met Ala Thr Val Leu Thr Gly Leu Ala Ile His Ser Ile Val	
1012	285 290 295 300	
1013		
1014	ATT CTC CCG CTG ATA TAT TTC ATA GTC GTA CGA AAG AAC CCT TTC CGA	963
1015	Ile Leu Pro Leu Ile Tyr Phe Ile Val Val Arg Lys Asn Pro Phe Arg	
1016	305 310 315	
1017		
1018	TTT GCC ATG GGA ATG GCC CAG GCT CTC CTG ACA GCT CTC ATG ATC TCT	1011
1019	Phe Ala Met Gly Met Ala Gln Ala Leu Leu Thr Ala Leu Met Ile Ser	
1020	320 325 330	

1021																		
1022	TCC	AGT	TCA	GCA	ACA	CTG	CCT	GTC	ACC	TTC	CGC	TGT	GCT	GAA	GAA	AAT		1059
1023	Ser	Ser	Ser	Ala	Thr	Leu	Pro	Val	Thr	Phe	Arg	Cys	Ala	Glu	Glu	Asn		
1024			335					340					345					
1025																		
1026	AAC	CAG	GTG	GAC	AAG	AGG	ATC	ACT	CGA	TTC	GTG	TTA	CCC	GTT	GGT	GCA		1107
1027	Asn	Gln	Val	Asp	Lys	Arg	Ile	Thr	Arg	Phe	Val	Leu	Pro	Val	Gly	Ala		
1028		350					355					360						
1029																		
1030	ACA	ATC	AAC	ATG	GAT	GGG	ACC	GCG	CTC	TAT	GAA	GCA	GTG	GCA	GCG	GTG		1155
1031	Thr	Ile	Asn	Met	Asp	Gly	Thr	Ala	Leu	Tyr	Glu	Ala	Val	Ala	Ala	Val		
1032	365					370					375					380		
1033																		
1034	TTT	ATT	GCA	CAG	TTG	AAT	GAC	CTG	GAC	TTG	GGC	ATT	GGG	CAG	ATC	ATC		1203
1035	Phe	Ile	Ala	Gln	Leu	Asn	Asp	Leu	Asp	Leu	Gly	Ile	Gly	Gln	Ile	Ile		
1036					385					390					395			
1037																		
1038	ACC	ATC	AGT	ATC	ACG	GCC	ACA	TCT	GCC	AGC	ATC	GGA	GCT	GCT	GGC	GTG		1251
1039	Thr	Ile	Ser	Ile	Thr	Ala	Thr	Ser	Ala	Ser	Ile	Gly	Ala	Ala	Gly	Val		
1040				400					405					410				
1041																		
1042	CCC	CAG	GCT	GGC	CTG	GTG	ACC	ATG	GTG	ATT	GTG	CTG	AGT	GCC	GTG	GGC		1299
1043	Pro	Gln	Ala	Gly	Leu	Val	Thr	Met	Val	Ile	Val	Leu	Ser	Ala	Val	Gly		
1044			415					420					425					
1045																		
1046	CTG	CCC	GCC	GAG	GAT	GTC	ACC	CTG	ATC	ATT	GCT	GTC	GAC	TGG	CTC	CTG		1347
1047	Leu	Pro	Ala	Glu	Asp	Val	Thr	Leu	Ile	Ile	Ala	Val	Asp	Trp	Leu	Leu		
1048		430					435					440						
1049																		
1050	GAC	CGG	TTC	AGG	ACC	ATG	GTC	AAC	GTC	CTT	GGT	GAT	GCT	TTT	GGG	ACG		1395
1051	Asp	Arg	Phe	Arg	Thr	Met	Val	Asn	Val	Leu	Gly	Asp	Ala	Phe	Gly	Thr		
1052	445					450					455					460		
1053																		
1054	GGC	ATT	GTG	GAA	AAG	CTC	TCC	AAG	AAG	GAG	CTG	GAG	CAG	ATG	GAT	GTT		1443
1055	Gly	Ile	Val	Glu	Lys	Leu	Ser	Lys	Lys	Glu	Leu	Glu	Gln	Met	Asp	Val		
1056					465					470					475			
1057																		
1058	TCA	TCT	GAA	GTC	AAC	ATT	GTG	AAT	CCC	TTT	GCC	TTG	GAA	TCC	ACA			

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/140,729ADATE: 03/04/94
TIME: 11:24:18

INPUT SET: S7433.raw

1072 525
1073
1074 AGTCATCTCA AACACGGCTT AAGGAAAAGA GAAA 1674
1075
1076
1077 (2) INFORMATION FOR SEQ ID NO:9:
1078
1079 (i) SEQUENCE CHARACTERISTICS:
1080 (A) LENGTH: 525 amino acids
1081 (B) TYPE: amino acid
1082 (D) TOPOLOGY: linear
1083
1084 (ii) MOLECULE TYPE: protein
1085
1086 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
1087
1088 Met Gly Lys Pro Ala Arg Lys Gly Cys Pro Ser Trp Lys Arg Phe Leu
1089 1 5 10 15
1090
1091 Lys Asn Asn Trp Val Leu Leu Ser Thr Val Ala Ala Val Val Leu Gly
1092 20 25 30
1093
1094 Ile Thr Thr Gly Val Leu Val Arg Glu His Ser Asn Leu Ser Thr Leu
1095 35 40 45
1096
1097 Glu Lys Phe Tyr Phe Ala Phe Pro Gly Glu Ile Leu Met Arg Met Leu
1098 50 55 60
1099
1100 Lys Leu Ile Ile Leu Pro Leu Ile Ile Ser Ser Met Ile Thr Gly Val
1101 65 70 75 80
1102
1103 Ala Ala Leu Asp Ser Asn Val Ser Gly Lys Ile Gly Leu Arg Ala Val
1104 85 90 95
1105
1106 Val Tyr Tyr Phe Cys Thr Thr Leu Ile Ala Val Ile Leu Gly Ile Val
1107 100 105 110
1108
1109 Leu Val Val Ser Ile Lys Pro Gly Val Thr Gln Lys Val Gly Glu Ile
1110 115 120 125
1111
1112 Ala Arg Thr Gly Ser Thr Pro Glu Val Ser Thr Val Asp Ala Met Leu
1113 130 135 140
1114
1115 Asp Leu Ile Arg Asn Met Phe Pro Glu Asn Leu Val Gln Ala Cys Phe
1116 145 150 155 160
1117
1118 Gln Gln Tyr Lys Thr Lys Arg Glu Glu Val Lys Pro Pro Ser Asp Pro
1119 165 170 175
1120
1121 Glu Met Asn Met Thr Glu Glu Ser Phe Thr Ala Val Met Thr Thr Ala
1122 180 185 190

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/140,729A

 DATE: 03/04/94
 TIME: 11:24:25
INPUT SET: S7433.raw

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1123
1124   Ile Ser Lys Asn Lys Thr Lys Glu Tyr Lys Ile Val Gly Met Tyr Ser
1125           195                      200                      205
1126
1127   Asp Gly Ile Asn Val Leu Gly Leu Ile Val Phe Cys Leu Val Phe Gly
1128       210                      215                      220
1129
1130   Leu Val Ile Gly Lys Met Gly Glu Lys Gly Gln Ile Leu Val Asp Phe
1131       225                      230                      235                      240
1132
1133
1134   Phe Asn Ala Leu Ser Asp Ala Thr Met Lys Ile Val Gln Ile Ile Met
1135           245                      250                      255
1136
1137   Cys Tyr Met Pro Leu Gly Ile Leu Phe Leu Ile Ala Gly Lys Ile Ile
1138           260                      265                      270
1139
1140   Glu Val Glu Asp Trp Glu Ile Phe Arg Lys Leu Gly Leu Tyr Met Ala
1141           275                      280                      285
1142
1143   Thr Val Leu Thr Gly Leu Ala Ile His Ser Ile Val Ile Leu Pro Leu
1144       290                      295                      300
1145
1146   Ile Tyr Phe Ile Val Val Arg Lys Asn Pro Phe Arg Phe Ala Met Gly
1147       305                      310                      315                      320
1148
1149   Met Ala Gln Ala Leu Leu Thr Ala Leu Met Ile Ser Ser Ser Ser Ala
1150           325                      330                      335
1151
1152   Thr Leu Pro Val Thr Phe Arg Cys Ala Glu Glu Asn Asn Gln Val Asp
1153           340                      345                      350
1154
1155   Lys Arg Ile Thr Arg Phe Val Leu Pro Val Gly Ala Thr Ile Asn Met
1156           355                      360                      365
1157
1158   Asp Gly Thr Ala Leu Tyr Glu Ala Val Ala Ala Val Phe Ile Ala Gln
1159       370                      375                      380
1160
1161   Leu Asn Asp Leu Asp Leu Gly Ile Gly Gln Ile Ile Thr Ile Ser Ile
1162       385                      390                      395                      400
1163
1164   Thr Ala Thr Ser Ala Ser Ile Gly Ala Ala Gly Val Pro Gln Ala Gly
1165           405                      410                      415
1166
1167   Leu Val Thr Met Val Ile Val Leu Ser Ala Val Gly Leu Pro Ala Glu
1168           420                      425                      430
1169
1170   Asp Val Thr Leu Ile Ile Ala Val Asp Trp Leu Leu Asp Arg Phe Arg
1171           435                      440                      445
1172
1173   Thr Met Val Asn Val Leu Gly Asp Ala Phe Gly Thr Gly Ile Val Glu

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/140,729ADATE: 03/04/94
TIME: 11:24:31

INPUT SET: S7433.raw

1174 450 455 460
1175
1176 Lys Leu Ser Lys Lys Glu Leu Glu Gln Met Asp Val Ser Ser Glu Val
1177 465 470 475 480
1178
1179 Asn Ile Val Asn Pro Phe Ala Leu Glu Ser Thr Ile Leu Asp Asn Glu
1180 485 490 495
1181
1182 Asp Ser Asp Thr Lys Lys Ser Tyr Val Asn Gly Gly Phe Ala Val Asp
1183 500 505 510
1184
1185
1186 Lys Ser Asp Thr Ile Ser Phe Thr Gln Thr Ser Gln Phe
1187 515 520 525
1188
1189

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGGGTACC GCCATGGAGA AGAGCAAC

28

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCGTCTAGA TCACAGAACC GACTCCTTG

29

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/140,729ADATE: 03/04/94
TIME: 11:24:37

INPUT SET: S7433.raw

1225
1226 (ii) MOLECULE TYPE: DNA (genomic)
1227
1228 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
1229
1230 CGCGGGTACC AATATGACTA AAAGCAATG 29
1231
1232 (2) INFORMATION FOR SEQ ID NO:13:
1233
1234 (i) SEQUENCE CHARACTERISTICS:
1235 (A) LENGTH: 29 base pairs
1236 (B) TYPE: nucleic acid
1237 (C) STRANDEDNESS: single
1238 (D) TOPOLOGY: linear
1239
1240 (ii) MOLECULE TYPE: DNA (genomic)
1241
1242 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
1243
1244 CGCGTCTAGA CTACATCTTG GTTTCAC TG 29
1245
1246 (2) INFORMATION FOR SEQ ID NO:14:
1247
1248 (i) SEQUENCE CHARACTERISTICS:
1249 (A) LENGTH: 29 base pairs
1250 (B) TYPE: nucleic acid
1251 (C) STRANDEDNESS: single
1252 (D) TOPOLOGY: linear
1253
1254 (ii) MOLECULE TYPE: DNA (genomic)
1255
1256 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
1257
1258 CGCGGGTACC ACCATGGCAT CTACGGAAG 29
1259
1260 (2) INFORMATION FOR SEQ ID NO:15:
1261
1262 (i) SEQUENCE CHARACTERISTICS:
1263 (A) LENGTH: 30 base pairs
1264 (B) TYPE: nucleic acid
1265 (C) STRANDEDNESS: single
1266 (D) TOPOLOGY: linear
1267
1268 (ii) MOLECULE TYPE: DNA (genomic)
1269
1270 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
1271
1272 CGCGTCTAGA TTATTTCTCA CGTTTCCAAG 30
1273
1274 (2) INFORMATION FOR SEQ ID NO:16:
1275

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/140,729ADATE: 03/04/94
TIME: 11:24:44

INPUT SET: S7433.raw

1276 (i) SEQUENCE CHARACTERISTICS:
1277 (A) LENGTH: 28 base pairs
1278 (B) TYPE: nucleic acid
1279 (C) STRANDEDNESS: single
1280 (D) TOPOLOGY: linear
1281
1282 (ii) MOLECULE TYPE: DNA (genomic)
1283
1284 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
1285
1286 CGCGGGTACC GCCATGGGGA AACCGGCG 28
1287
1288 (2) INFORMATION FOR SEQ ID NO:17:
1289
1290 (i) SEQUENCE CHARACTERISTICS:
1291 (A) LENGTH: 28 base pairs
1292 (B) TYPE: nucleic acid
1293 (C) STRANDEDNESS: single
1294 (D) TOPOLOGY: linear
1295
1296 (ii) MOLECULE TYPE: DNA (genomic)
1297
1298 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
1299
1300 CGCGGGATCC CTAGAACTGT GAGGTCTG 28
1301

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/140,729A

DATE: 03/04/94
TIME: 11:24:47

INPUT SET: S7433.raw

Line

Error

Original Text

ENTERED

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/08/140,729A

DATE: 03/04/94
TIME: 11:24:47

INPUT SET: S7433.raw

APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/08/140,729A

DATE: 03/04/94
TIME: 11:24:48

INPUT SET: S7433.raw

Line	Original Text	Corrected Text
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